

RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/09/462,682

TIME: 16:00:20

Input Set : A:\Nih310-1.app

Output Set: N:\CRF3\07252001\I462682.raw

ENTERED

3 <110> APPLICANT: FitzGerald, David J.
 4 The Government of the United States of America
 5 as represented by the Secretary,
 6 Department of Health and Human Services
 8 <120> TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
 10 <130> FILE REFERENCE: 015280-310100US
 12 <140> CURRENT APPLICATION NUMBER: US 09/462,682
 C--> 13 <141> CURRENT FILING DATE: 2001-07-13
 15 <150> PRIOR APPLICATION NUMBER: US 60/052,375
 16 <151> PRIOR FILING DATE: 1997-07-11
 18 <150> PRIOR APPLICATION NUMBER: WO PCT/US98/14341
 19 <151> PRIOR FILING DATE: 1998-07-10
 21 <160> NUMBER OF SEQ ID NOS: 13
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1839
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Pseudomonas aeruginosa
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(1839)
 33 <223> OTHER INFORMATION: exotoxin A
 35 <400> SEQUENCE: 1
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 37 Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
 38 1 5 10 15
 40 ctc gac ctc aag gac ggc gtg cgt tcc agc cgc atg agc gtc gac ccg 96
 41 Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
 42 20 25 30
 44 gcc atc gcc gac acc aac ggc cag ggc gtg ctg cac tac tcc atg gtc 144
 45 Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
 46 35 40 45
 48 ctg gag ggc ggc aac gac gcg ctc aag ctg gcc atc gac aac gcc ctc 192
 49 Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
 50 50 55 60
 52 agc atc acc agc gac ggc ctg acc atc cgc ctc gaa ggc ggc gtc gag 240
 53 Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
 54 65 70 75 80
 56 ccg aac aag ccg gtg cgc tac agc tac acg cgc cag gcg cgc ggc agt 288
 57 Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
 58 85 90 95
 60 tgg tcg ctg aac tgg ctg gta ccg atc ggc cac gag aag ccc tcg aac 336
 61 Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
 62 100 105 110
 64 atc aag gtg ttc atc cac gaa ctg aac gcc ggc aac cag ctc agc cac 384
 65 Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
 66 115 120 125

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68 atg tcg ccg atc tac acc atc gag atg ggc gac gag ttg ctg gcg aag 432
69 Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
70 130 135 140
72 ctg gcg cgc gat gcc acc ttc ttc gtc agg gcg cac gag agc aac gag 480
73 Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
74 145 150 155 160
76 atg cag ccg acg ctc gcc atc agc cat gcc ggg gtc agc gtg gtc atg 528
77 Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
78 165 170 175
80 gcc cag acc cag ccg cgc cgg gaa aag cgc tgg agc gaa tgg gcc agc 576
81 Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
82 180 185 190
84 ggc aag gtg ttg tgc ctg ctc gac ccg ctg gac ggg gtc tac aac tac 624
85 Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
86 195 200 205
88 ctc gcc cag caa cgc tgc aac ctc gac gat acc tgg gaa ggc aag atc 672
89 Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
90 210 215 220
92 tac cgg gtg ctc gcc ggc aac ccg gcg aag cat gac ctg gac atc aaa 720
93 Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
94 225 230 235 240
96 ccc acg gtc atc agt cat cgc ctg cac ttt ccc gag ggc ggc agc ctg 768
97 Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
98 245 250 255
100 gcc gcg ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag act ttc 816
101 Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
102 260 265 270
104 acc cgt cat cgc cag ccg cgc ggc tgg gaa caa ctg gag cag tgc ggc 864
105 Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
106 275 280 285
108 tat ccg gtg cag cgg ctg gtc gcc ctc tac ctg gcg gcg ccg ctg tcg 912
109 Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
110 290 295 300
112 tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc ccc ggc 960
113 Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
114 305 310 315 320
116 agc ggc ggc gac ctg ggc gaa gcg atc cgc gag cag ccg gag cag gcc 1008
117 Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
118 325 330 335
120 cgt ctg gcc ctg acc ctg gcc gcc gcc gag agc gag cgc ttc gtc ccg 1056
121 Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
122 340 345 350
124 cag ggc acc ggc aac gac gag gcc ggc gcg gcc aac gcc gac gtg gtg 1104
125 Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val
126 355 360 365
128 agc ctg acc tgc ccg gtc gcc gcc ggt gaa tgc gcg ggc ccg gcg gac 1152
129 Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp
130 370 375 380
132 agc ggc gac gcc ctg ctg gag cgc aac tat ccc act ggc gcg gag ttc 1200

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133 Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe
134 385                      390                      395                      400
136 ctc ggc gac ggc ggc gac gtc agc ttc agc acc cgc ggc acg cag aac      1248
137 Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn
138                      405                      410                      415
140 tgg acg gtg gag cgg ctg ctc cag gcg cac cgc caa ctg gag gag cgc      1296
141 Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg
142                      420                      425                      430
144 ggc tat gtg ttc gtc ggc tac cac ggc acc ttc ctc gaa gcg gcg caa      1344
145 Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln
146                      435                      440                      445
148 agc atc gtc ttc ggc ggg gtg cgc gcg cgc agc cag gac ctc gac gcg      1392
149 Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala
150                      450                      455                      460
152 atc tgg cgc ggt ttc tat atc gcc ggc gat ccg gcg ctg gcc tac ggc      1440
153 Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly
154 465                      470                      475                      480
156 tac gcc cag gac cag gaa ccc gac gca cgc ggc cgg atc cgc aac ggt      1488
157 Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly
158                      485                      490                      495
160 gcc ctg ctg cgg gtc tat gtg ccg cgc tcg agc ctg ccg ggc ttc tac      1536
161 Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr
162                      500                      505                      510
164 cgc acc agc ctg acc ctg gcc gcg ccg gag gcg gcg ggc gag gtc gaa      1584
165 Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu
166                      515                      520                      525
168 cgg ctg atc ggc cat ccg ctg ccg ctg cgc ctg gac gcc atc acc ggc      1632
169 Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly
170                      530                      535                      540
172 ccc gag gag gaa ggc ggg cgc ctg gag acc att ctc ggc tgg ccg ctg      1680
173 Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu
174 545                      550                      555                      560
176 gcc gag cgc acc gtg gtg att ccc tcg gcg atc ccc acc gac ccg cgc      1728
177 Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
178                      565                      570                      575
180 aac gtc ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag gaa cag      1776
181 Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
182                      580                      585                      590
184 gcg atc agc gcc ctg ccg gac tac gcc agc cag ccc ggc aaa ccg ccg      1824
185 Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
186                      595                      600                      605
188 cgc gag gac ctg aag
189 Arg Glu Asp Leu Lys
190                      610
193 <210> SEQ ID NO: 2
194 <211> LENGTH: 613
195 <212> TYPE: PRT
196 <213> ORGANISM: Pseudomonas aeruginosa
198 <400> SEQUENCE: 2

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199 Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
200 1 5 10 15
202 Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
203 20 25 30
205 Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
206 35 40 45
208 Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
209 50 55 60
211 Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
212 65 70 75 80
214 Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
215 85 90 95
217 Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
218 100 105 110
220 Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
221 115 120 125
223 Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
224 130 135 140
226 Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
227 145 150 155 160
229 Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
230 165 170 175
232 Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
233 180 185 190
235 Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
236 195 200 205
238 Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
239 210 215 220
241 Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
242 225 230 235 240
244 Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
245 245 250 255
247 Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
248 260 265 270
250 Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
251 275 280 285
253 Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
254 290 295 300
256 Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
257 305 310 315 320
259 Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
260 325 330 335
262 Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
263 340 345 350
265 Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val
266 355 360 365
268 Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp
269 370 375 380
271 Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe

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272 385          390          395          400
274 Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn
275          405          410          415
277 Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg
278          420          425          430
280 Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln
281          435          440          445
283 Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala
284          450          455          460
286 Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly
287 465          470          475          480
289 Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly
290          485          490          495
292 Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr
293          500          505          510
295 Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu
296          515          520          525
298 Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly
299          530          535          540
301 Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu
302 545          550          555          560
304 Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
305          565          570          575
307 Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
308          580          585          590
310 Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
311          595          600          605
313 Arg Glu Asp Leu Lys
314          610
318 <210> SEQ ID NO: 3
319 <211> LENGTH: 35
320 <212> TYPE: PRT
321 <213> ORGANISM: Human immunodeficiency virus type 1
323 <220> FEATURE:
324 <221> NAME/KEY: PEPTIDE
325 <222> LOCATION: (1)..(35)
326 <223> OTHER INFORMATION: V3 loop of MN strain of HIV-1
328 <400> SEQUENCE: 3
329 Cys Thr Arg Pro Asn Tyr Asn Lys Arg Lys Arg Ile His Ile Gly Pro
330 1          5          10          15
332 Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr Ile Arg Gln
333          20          25          30
335 Ala His Cys
336          35
339 <210> SEQ ID NO: 4
340 <211> LENGTH: 35
341 <212> TYPE: PRT
342 <213> ORGANISM: Human immunodeficiency virus type 1
344 <220> FEATURE:

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VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date